

Resource Summary Report

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UniRef

RRID:SCR_010646

Type: Tool

Proper Citation

UniRef (RRID:SCR_010646)

Resource Information

URL: <http://www.uniprot.org/help/uniref>

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Description: Databases which provide clustered sets of sequences from UniProt Knowledgebase and selected UniParc records, in order to obtain complete coverage of sequence space at several resolutions while hiding redundant sequences from view. The UniRef100 database combines identical sequences and sub-fragments with 11 or more residues (from any organism) into a single UniRef entry. The sequence of a representative protein, the accession numbers of all the merged entries, and links to the corresponding UniProtKB and UniParc records are all displayed in the entry. UniRef90 and UniRef50 are built by clustering UniRef100 sequences with 11 or more residues such that each cluster is composed of sequences that have at least 90% (UniRef90) or 50% (UniRef50) sequence identity to the longest sequence (UniRef seed sequence). All the sequences in each cluster are ranked to facilitate the selection of a representative sequence for the cluster.

Synonyms: UniProt Reference Clusters

Resource Type: data or information resource, database

Defining Citation: [PMID:17379688](#)

Keywords: database, protein sequence, sub-fragment, sequence cluster, clustered set

Funding: NHGRI U01 HG02712

Availability: Updated biweekly

Resource Name: UniRef

Resource ID: SCR_010646

Alternate IDs: nlx_66133, r3d100011518

Record Creation Time: 20220129T080259+0000

Record Last Update: 20260905T133159+0000

Ratings and Alerts

No rating or validation information has been found for UniRef.

No alerts have been found for UniRef.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 309 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Ding K, et al. (2026) Deconvolving mutation effects on protein stability and function with disentangled protein language models. bioRxiv : the preprint server for biology.

Diotallevi M, et al. (2026) iNOS modulates inflammatory responses in an NO-independent manner through direct interaction with IRG1 in mitochondria. Nature metabolism, 8(4), 855.

Stevenson Z, et al. (2026) Lowering the Mo limit for nitrogen fixation by Mo-nitrogenase. Communications earth & environment, 7(1), 169.

Ali F, et al. (2026) A generative explainable model for antimicrobial peptide prediction using bidirectional temporal convolutional neural network. Scientific reports, 16(1).

Elreify HM, et al. (2026) BiGKbhb: a bi-directional gated recurrent unit model for predicting lysine ??-hydroxybutyrylation sites. BMC genomics, 27(1), 102.

Chellappan BV, et al. (2026) Computational Modeling of Cellulose Synthase Heterotrimer Assembly and Identification of Antimicrobial Compounds Targeting Interface Sites in Phytophthora infestans. Journal of fungi (Basel, Switzerland), 12(3).

Ettema TW, et al. (2026) Shared structural mechanisms of alternating access between the secondary peptide transporter SbmA and ABC transporters. Nature communications, 17(1).

Shoombuatong W, et al. (2026) NToxSEM: Enhancing prediction of neurotoxic peptides and neurotoxins using a stacked ensemble-based multimodal framework. Protein science : a publication of the Protein Society, 35(7), e70661.

He Z, et al. (2026) Effects of Rice Straw Incorporation on Paddy Soil Microbiome and Metabolome Throughout the Crop Growth Period. Microorganisms, 14(6).

Muhaiminul Islam Nafi M, et al. (2026) Predicting protein-carbohydrate binding sites: a deep learning approach integrating protein language model embeddings and structural features. *Briefings in bioinformatics*, 27(1).

Lee H, et al. (2026) Protein folding stability estimation with explicit consideration of unfolded states. *Nature communications*, 17(1).

Chowdhury SF, et al. (2026) Metatranscriptomic insights into host-microbiome interactions underlying asymptomatic COVID-19 cases. *Scientific reports*, 16(1).

Manzano-Morales S, et al. (2026) Phylogenomics of Asgard archaea reveals a unique blend of prokaryotic-like horizontal transfer and eukaryotic-like gene duplication. *Nature communications*, 17(1).

Ali F, et al. (2026) DeepStackVEGF a stacking ensemble deep learning framework for vascular endothelial growth factor prediction. *Scientific reports*, 16(1).

Li J, et al. (2026) Mechanism-Driven Screening of Membrane-Targeting and Pore-Forming Antimicrobial Peptides. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(9), e16470.

Chen L, et al. (2026) Root-associated protein prediction using a protein large language model and hypergraph convolutional networks. *Scientific reports*, 16(1), 4876.

Kerr EN, et al. (2026) Interactions of Mucus Monosaccharides and the Epidermal Microbiome in Four Benthic Elasmobranchs. *Environmental microbiology reports*, 18(2), e70303.

Pei SC, et al. (2026) Comparative genomics of a poinsettia-associated phytoplasma and functional validation of its SAP11-homologous effectors that induce plant branching. *Microbial genomics*, 12(3).

Rathwell C, et al. (2026) Hi-C Links Reveal Viral Activity and Infection Within the Free-Living Microbial Community of a Secondary Chlorophyll Maximum in the Eastern Tropical North Pacific. *Environmental microbiology*, 28(4), e70274.

Cao H, et al. (2026) Characterization of the gastric mucosal microbiota in tumoral and peritumoral mucosa in patients with advanced gastric cancer from Northwest China. *Frontiers in microbiology*, 17, 1763714.